

EXHIBIT 5
(PART 4 OF 4)

Table 4. Markers that were Under-expressed in Ovarian Cancer in a Comparison of Ovarian Epithelial Cancer to Normal Postmenopausal Ovarian Tissue

SEQ. ID. NO.	IMAGE ID	Nucleic Acid	Description	Average log normal	Average log cancer	Cancer to normal
202	878596	ITM2A	integral membrane protein 2A	1.145	-2.036	0.110
203-204	42558	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	4.137	0.945	0.109
205-207	81417	RNASE4	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	2.057	-0.744	0.144
208-210	471642	LAMA2	laminin alpha 2 (merosin, congenital muscular dystrophy)	2.806	0.361	0.184
211	448386	PBX3	pre-B-cell leukemia transcription factor 3	2.354	-0.243	0.165
212	1472538	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	2.604	0.099	0.176
213	814636	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	3.055	0.231	0.141
214-215	488956	CUGBP2	CUG triplet repeat, RNA-binding protein 2	2.960	-0.043	0.125
216-218	209655	TGFBR3	TGF beta receptor type III	1.956	0.057	0.268
219	859858	STAR	steroidogenic acute regulatory protein	1.685	0.026	0.317
220	1636447	GNG11	guanine nucleotide binding protein 11	1.683	-0.953	0.161
221	491565	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.576	-0.497	0.238
222	744647	CTNNA1	catenin (cadherin-associated protein), alpha-like 1	1.498	-0.761	0.209
223	743773	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	2.317	0.060	0.209
224-226	188232	KLF4	GKLF=EZF=KLF4=gut-enriched Kruppel-like zinc finger protein=expressed in vascular endothelial cells	1.644	-0.741	0.191
227-228	471725	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	1.600	-0.616	0.215
229-230	487793	MAF	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog	0.765	-2.032	0.144
231-232	768370	FOXC1	forkhead box C1	2.270	-0.021	0.204
233	461351	TCF21	transcription factor 21	1.733	0.193	0.344
234-236	248295	CCNI	Cyclin I	2.460	-0.030	0.178
237-238	209367	DCN	decorin	3.762	0.582	0.110
239-240	789049	CBF2	CCAAT-box-binding transcription factor	2.140	0.019	0.230

241-242	68049		Homo sapiens, clone IMAGE:4183312, mRNA, partial cds	2.074	0.243	0.281
122	81417	RNASE4	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	1.696	-0.117	0.285
243	2094012	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adapter protein	1.869	0.195	0.313
244-245	377731	GSTM5	glutathione S-transferase M5	1.558	0.242	0.402
246	460470	C4BPB	complement component 4-binding protein, beta	0.750	-0.851	0.330
247-248	73609	HS3ST1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.017	0.328	0.310
249	2413955	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	2.739	0.465	0.207
250	897823	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	1.703	-0.229	0.262
251	1558799	CIRBP	cold inducible RNA-binding protein	1.817	-0.183	0.250
252	2321596	RGS2	regulator of G-protein signalling 2, 24kD	1.607	-0.290	0.269
253-254	786607	TCEAL1	transcription elongation factor A (SII)-like 1	1.737	0.083	0.318
255-256	377461	CAV1	caveolin 1, caveolae protein, 22kD	0.146	-2.506	0.159
257	855624	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	2.030	-0.068	0.233
258-259	343443	RBPMS	RNA-binding protein gene with multiple splicing	1.727	-0.240	0.256
260-261	62263	ADAMTS1	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	1.589	0.029	0.339
262-263	51408	DSCR1L1	Down syndrome critical region gene 1-like 1	2.054	0.260	0.288
264	436121	DLK1	delta-like homolog (Drosophila)	0.307	-1.944	0.210
265-266	491113	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	2.308	0.502	0.286
139	840776	SGK	sgk=putative serine/threonine protein kinase transcriptionally modified during anisotonic and isotonic alterations of cell volume	1.444	-0.201	0.320
267	450060	HFL1	H factor (complement)-like 1	2.490	0.664	0.282
268-269	38347	FOG2	Friend of GATA2	1.905	0.463	0.368
270	898122	C7	complement component 7	2.643	0.660	0.253
271-272	784109	SGCE	sarcoglycan, epsilon	1.573	-0.213	0.290
273	898305	NBL1	neuroblastoma, suppression of tumorigenicity 1	1.910	0.153	0.296
274-275	173385	HBB	hemoglobin, beta	0.165	-2.317	0.179
276-278	840683	CARP	Cytokine inducible nuclear protein	1.728	0.018	0.306
279-280	278570	MITF	microphthalmia-associated transcription factor	0.242	-1.580	0.283
281-282	898062	CDC20	p55CDC	1.679	-0.043	0.303
283-285	148028	EPS8	epidermal growth factor receptor kinase substrate (Eps8)	1.595	-0.344	0.261

286-287	345680	ARHI	ras homolog gene family, member I	1.595	0.212	0.383
288	857002	B4-2	proline-rich protein with nuclear targeting signal	1.523	0.285	0.424
289-291	186132	SELE	ELAM1=endothelial leukocyte adhesion molecule I	1.480	-0.393	0.273
292-293	133273	PMP22	peripheral myelin protein 22	1.767	0.017	0.297
294	340657	EBAF	endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfamily)	1.422	-0.076	0.354
295-296	609663	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	1.357	-0.461	0.284
297	1573311	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	1.242	-1.102	0.197
298-299	269806	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	2.324	0.315	0.248
158	309864	JUNB	jun B proto-oncogene	3.465	1.117	0.196
300	1573108	BCKDK	branched chain alpha-ketoacid dehydrogenase kinase	1.306	-1.057	0.194
301-303	298268	BTG1	BTG1=B-cell translocation gene 1=anti-proliferative	1.409	-0.239	0.319
304-305	784772	AKAP12	A kinase (PRKA) anchor protein (gravin) 12	1.568	-0.413	0.253
306-307	898221	NR4A2	NOT=Immediate early response protein=Nurr1 homologue=Nurr77 orphan steroid receptor family member	2.092	0.341	0.297
308-309	126531	HBB	hemoglobin, beta	0.190	-2.034	0.214
310-311	768489	ARHGAP6	Rho GTPase activating protein 6	1.263	-0.109	0.386
312	1568391	PLS3	plastin 3 (T isoform)	1.241	-1.045	0.205
313-314	300015	FNTA	farnesyltransferase, CAAX box, alpha	1.354	0.091	0.417
315-316	770670	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	2.088	0.445	0.320
317-318	840944	EGR1	early growth response 1	3.245	0.765	0.179
319	795213	RNAC	RNA cyclase homolog	1.812	0.043	0.293
320	813584	PA26	p53 regulated PA26 nuclear protein	1.329	0.084	0.422
321	1573778	C11orf13	chromosome 11 open reading frame 13	1.241	-1.048	0.205
322	2169465	ING1L	inhibitor of growth family, member 1-like	1.267	0.031	0.425
323	2577249	RPL9	ribosomal protein L9	1.756	-0.313	0.238
324-325	813711	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	1.211	-0.616	0.282
326-327	298122	FZD7	frizzled (Drosophila) homolog 7	2.554	0.747	0.286
328-329	366100	MATN2	matrilin 2	2.205	0.536	0.315
330-331	71863	SLC11A3	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	2.466	0.808	0.317
332-333	767641		ESTs	0.965	-0.153	0.461
334-335	292463	ERCC5	excision repair cross-complementing rodent repair deficiency, complementation	1.695	-0.098	0.289

Table 5. Markers that were Over-expressed in Ovarian Cancer in a Comparison of Ovarian Epithelial Cancer to Normal Postmenopausal Ovarian Tissue

SEQ. ID. NO.	IMAGE ID	Nucleic Acid	Description	Average log normal	Average log cancer	Cancer to normal
18-19	82195	SERPINF2	Branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)		1.45	
30-31	295939	FLJ22174	hypothetical protein FLJ22174		1.38	
50-51	755599	IFITM1	Interferon induced transmembrane protein 1 (9-27)		1.74	
55-57	624655	IFITM2	Interferon-induced protein 1-8D		1.53	
60	786675	HE4	Epididymis-specific, whey-acidic protein type, four-disulfide core; putative ovarian carcinoma marker		2.41	
68-69	782513	G1P3	Interferon, alpha-inducible protein (clone IFI-6-16)		1.64	
74-76	182288	DDR1	Receptor protein-tyrosine kinase EDDR1		1.43	
85-86	811139	HLA-DRB5	Major histocompatibility complex, class II, DR beta 5		1.91	
101-103	417711	HLA-DRB1	Major histocompatibility complex, class II, DR beta 1		1.94	
89-91	725751	CD74	Invariant chain=la-associated invariant gamma-chain		2.69	
92-93	840681	CD74	Invariant chain=la-associated invariant gamma-chain		2.58	
94-96	117411	HLA-DRA	MHC Class II=DR alpha		1.62	
97-99	207715	HLA-DPA	MHC Class II=DP alpha		1.85	
122-123	361323	RGS1	regulator of G-protein signaling 1		1.73	
133-135	755279	FOS	c-fos		1.76	
149-151	279388	SORL1	Mosaic protein LR11=hybrid receptor gp250 precursor		1.56	
164-166	813256	ABCB1	MDR1=Multidrug resistance protein 1=P-glycoprotein		1.64	
167-168	23804	ZFP36	Zinc finger protein homologous to Zfp-36 in mouse		1.74	
169-171	135880	ZFP36	TTP=tristetraproline=GOS24=zinc finger transcriptional regulator		2.00	
174-175	41650	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)		1.54	
176-178	840776	SGK	sgk=putative serine/threonine protein kinase transcriptionally modified during anisotonic and isotonic alteration		2.02	
179-180	814508	PPP1R7	Protein phosphatase 1, regulatory subunit 7		1.78	
181-182	204335	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)		2.75	

190-192	485770	BRF2	Tis 11d=ERF-2=growth factor early response gene		1.62	
199-201	144675	TLR3	TLR3= Toll-like receptor 3		1.98	
340-341	378813	SLPI	secretory leukocyte protease inhibitor (antileukoproteinase)	-0.379	2.294	6.377
342	378461	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-2.657	-0.088	5.938
343-344	741977	BF	B-factor, properdin	-0.362	1.953	4.974
345-347	810899	CKS1	ckshs1=homolog of Cks1=p34Cdc28/Cdc2-associated protein	-1.484	0.637	4.351
348-349	470393	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	0.673	2.535	3.635
350-351	742101	PAX8	paired box gene 8	-0.566	1.196	3.391
352-353	814378	SPINT2	serine protease inhibitor, Kunitz type, 2	-0.306	1.432	3.336
354	451907	ZWINT	ZW10 interactor	-2.461	-0.856	3.043
355	2544675	DGKH	diacylglycerol kinase, eta	-0.036	1.498	2.896
356	782811	HMG1Y	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	-2.272	-0.760	2.851
357-359	504763	SDC4	Syndecan-4 = amphiglycan = ryudocan core protein	-0.871	0.575	2.725
360	1161155	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	-0.839	0.593	2.699
361-362	810873	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	0.127	1.534	2.652
363	43550	LDHA	lactate dehydrogenase A	-3.496	-2.152	2.538
364-365	131839	FOLR1	folate receptor 1 (adult)	-0.867	0.467	2.522
366-367	855749	TPI1	Triosephosphate isomerase 1	-2.272	-1.008	2.400
368	2514426	KLK8	kallikrein 8 (neuropsin/ovasin)	-0.491	0.742	2.352
200	79629	CXCR4	CXC chemokine receptor 4= fusin=neuropeptide Y receptor=L3	-0.588	0.618	2.307
369-370	825606	KNSL1	kinesin-like 1	-1.797	-0.602	2.290
371-372	488964	H2AFO	H2A histone family, member O	-1.329	-0.144	2.274
373-374	153411	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.967	3.150	2.270
375	1323448	CRIP1	cysteine-rich protein 1 (intestinal)	0.086	1.246	2.234
376	950700	PP	pyrophosphatase (inorganic)	-1.029	0.118	2.214
377-378	666391	ESTs	Unknown	0.214	1.360	2.212
379-381	207358	SLC2A1	glucose transporter (HepG2)	-1.190	-0.050	2.204
382	897770	ESTs	Unknown	-0.173	0.943	2.167
383-385	813673	HDGF	hepatoma-derived growth factor	-0.786	0.329	2.166
386	882522	ASS	argininosuccinate synthetase	-0.424	0.676	2.143
387-388	770388	CLDN4	claudin 4	0.065	1.159	2.135
389	897956	PRAME	preferentially expressed antigen in melanoma	-2.071	-0.977	2.134
390-391	897788	PTPRF	LAR = LCA-homologue	-0.175	0.900	2.108
392-393	741139	EYA2	eyes absent (Drosophila) homolog 2	-0.133	0.939	2.102
394-396	138917	MYCL1	L-myc	-0.042	1.026	2.096
397-399	840691	STAT1	STAT1=IFN alpha/beta-responsive transcription factor	-0.023	1.044	2.095

			ISGF3 beta subunits (p91/p84)			
400-401	564492	MTCH2	mitochondrial carrier homolog 2	-1.566	-0.512	2.076
402	435597	HTR3A	5-hydroxytryptamine (serotonin) receptor 3A	-0.392	0.656	2.067
403-404	68950	CCNE1	cyclin E1	-0.470	0.577	2.066
405	739155	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	-0.286	0.748	2.048
406-408	531028	PRKAG1	5'-AMP-activated protein kinase, gamma-1 subunit	0.148	1.181	2.046
409	2403485	DEFB1	defensin, beta 1	0.335	1.357	2.031
410-411	626502	ARPC1B	actin related protein 2/3 complex, subunit 1A (41 kD)	-0.808	0.213	2.030
412-414	71622	PRKCI	PKC iota=Protein kinase C, iota	-0.202	0.802	2.006
415	1610448	GAPD	glyceraldehyde-3-phosphate dehydrogenase	-1.484	-0.480	2.005
416-417	85497	C2	complement component 2	-0.413	0.589	2.002
418-419	843075	H2AFY	H2A histone family, member Y	-0.829	0.164	1.990
420-421	840567	TM4SF1	transmembrane 4 superfamily member 1	-1.261	-0.270	1.987
422-423	50117	GAPD	glyceraldehyde-3-phosphate dehydrogenase	-2.692	-1.706	1.981
424-426	809910	IFITM3	Interferon-inducible protein 1-8U	-0.099	0.887	1.981
427-428	248261	GLDC	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)	-0.757	0.221	1.970
429-430	144881	CALU	calumenin	-1.579	-0.620	1.943
431-432	208764	HBA2	hemoglobin, alpha 2	-0.114	0.837	1.934
433	810612	S100A11	S100 calcium-binding protein A11 (calgizzarin)	-0.670	0.279	1.931
434-436	897567	LDHA	Lactate dehydrogenase A	-2.982	-2.038	1.925
437	769921	UBE2C	ubiquitin-conjugating enzyme E2C	-1.429	-0.487	1.922
438-440	304908	E2F3	E2F-3=pRB-binding transcription factor=KIAA0075	-0.526	0.416	1.921
441-442	251019	CDH1	E-cadherin	-0.248	0.682	1.905
443-444	210405	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	-0.715	0.213	1.902
445-447	344430	BMP7	OP-1=osteogenic protein in the TGF-beta family	-0.075	0.852	1.901
448	825470	TOP2A	TOP2A			2

Table 6. Markers that were Differentially Expressed Between *BRCA1*-Linked and Sporadic Tumors in a Comparison to reference Immortalized Ovarian Epithelial Cells.

SEQ ID NO.	Nucleic Acid	Description	Geometric mean of ratios in BRCA1	Geometric mean of ratios in sporadic	Fold difference in geometric means
805	CD72	B-cell differentiation antigen CD72 (human);	1.49	1.17	0.79
544	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	1.27	1.08	0.84
545-547	LCN2	lipocalin 2 (oncogene 24p3)	1.29	0.98	0.76
538-540	PSTPIP1	interferon-gamma IEF SSP 5111; Interferon gamma upregulated protein	1.95; 1.6	1.31; 1.04	0.67; 0.65
543	SIAHBP1	fuse-binding protein-interacting repressor	1.86	1.21	0.65
533	UBE1	ubiquitin-activating enzyme E1	1.54	0.94	0.61
524-526	WAS	Wiskott-Aldrich syndrome protein	1.13	0.79	0.7
541-542	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.69	1.02	0.6
527-528	PCTK1	PCTAIRE 1 serine/threonine protein kinase	1.33	1.12	0.84

Table 7. Markers that were Differentially Expressed Between *BRCA2*-Linked and Sporadic Tumors in a Comparison to reference Immortalized Ovarian Epithelial Cells.

SEQ ID NO.	Nucleic Acid	Description	Geometric mean of ratios in BRCA1-linked tumors	Geometric mean of ratios in sporadic tumors	Fold difference in geometric means
279	LOC51760	B/K protein	1.32	1.1	0.83
280	LRPAP1	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	1.45	1.13	0.78

Table 8. Markers that were Differentially Expressed Between Combined *BRCA*-Linked Group and Sporadic Tumors in a Comparison to reference Immortalized Ovarian Epithelial Cells.

SEQ ID NO.	Nucleic Acid	Description	Geometric mean of ratios in BRCA1-linked tumors	Geometric mean of ratios in sporadic tumors	Fold difference in geometric means
281	PSTPIP1	interferon-gamma IEF SSP 5111=Interferon gamma upregulated protein	1.73; 1.41	1.31; 1.04	0.76; 0.74
282	IDH2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	1.66	1.02	0.61
274	PCTK1	PCTAIRE 1 serine/threonine protein kinase	1.29	1.12	0.86

Table 9. Markers that were Differentially Expressed between *BRCA1*-like and *BRCA2*-like tumors in a Comparison to reference Immortalized Ovarian Epithelial Cells.

SEQ ID NO:	Gene	Description	Geometric mean of ratios in BRCA1	Geometric mean of ratios in BRCA2	Fold Difference in Geometric Means
122-123	RGS1	regulator of G-protein signalling 1	1.79	4.75	2.65
122-123	RGS1	BL34=RGS1=regulator of G-protein signaling which inhibits SDF-1 directed B cell migration	2.09	5.05	2.41
594-596	RGS16	A28-RGS14p=G protein signaling regulator	1.22	2.32	1.9
612-614	SCYA4	MIP-1 beta=SCAY2=G-26=HC21=pAT 744=LAG-1=Act-2=H400=SIS-gamma=chemokine	1.29	2.23	1.73
612-614	SCYA4	MIP-1 beta=SCAY2=G-26=HC21=pAT 744=LAG-1=Act-2=H400=SIS-gamma=chemokine	1.09	1.79	1.64
515-517	SFRP4	frizzled related protein frpHE	1.13	1.85	1.63
594-596	RGS16	A28-RGS14p=G protein signaling regulator	1.33	2.11	1.58
790-791	APEX	APEX nuclease (multifunctional DNA repair enzyme)	0.66	1.04	1.58
682	SFRS11	splicing factor, arginine/serine-rich 11	0.69	1.09	1.57
507-509	PTEN	MMAC1=PTEN=Tumor suppressor gene at 10q23.3 that is Mutated in Multiple Advanced Cancers=Phosphatase and	1.03	1.56	1.51

		tensin homolog			
774	PDE6A	phosphodiesterase 6A, cGMP-specific, rod, alpha	1.23	1.85	1.51
562-564	CD83	CD83=B-G antigen IgV domain homolog=B-cell activation protein=HB15	1.46	2.19	1.5
592-593	ZFP161	ZF5=POZ domain zinc finger protein	1.03	1.49	1.45
		ESTs	1.17	1.69	1.44
707-708	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	1.38	1.93	1.4
762	FLJ10701	hypothetical protein FLJ10701	1	1.4	1.39
577-579	CD36	CD36	1.32	1.82	1.38
797-799	WNT2	Wnt-2	0.81	1.12	1.38
		Unknown	0.82	1.13	1.38
779	TCF4	transcription factor 4	1.19	1.62	1.36
615-617	KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	0.8	1.08	1.35
		ESTs	0.81	1.09	1.35
534-535	LOC51760	B/K protein	0.98	1.32	1.35
797-799	WNT2	Wnt-2	0.99	1.33	1.34
683-684	CUGBP1	CUG triplet repeat, RNA-binding protein 1	0.73	0.98	1.33
709	CSRP2	cysteine and glycine-rich protein 2	0.98	1.31	1.33
		ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	0.81	1.06	1.32
606-608	MMP13	MMP-13=Matrix metalloproteinase 13=CL-3=Collagenase 3	0.99	1.3	1.32
580-582	PDGFRB	Platelet-derived growth factor receptor, beta polypeptide=fused to TEL in t(5;12)(q33;p13) chronic myelomonocytic leukemia	1.41	1.85	1.31
603-605	ENPP1	PC-1 = alkaline nucleotide pyrophosphatase	1.01	1.32	1.31
		FGFR2=Fibroblast growth factor receptor 2	0.8	1.05	1.31
695-696	SMG1	PI-3-kinase-related kinase SMG-1	1.07	1.4	1.31
521-523	TAL1	scl=tal-1=T-cell acute lymphocytic leukemia 1	1.14	1.49	1.31
727-728	PLXNA2	plexin A2	1.32	1.71	1.3
759	LOC51605	CGI-09 protein	0.8	1.04	1.3
784	TNRC12	trinucleotide repeat containing 12	1.02	1.33	1.3

		EST	0.86	1.12	1.3
797-799	WNT2	wingless-type MMTV integration site family member 2	0.98	1.27	1.29
693-694	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A (220kD)	0.79	1.01	1.29
737-738	FLJ21661	hypothetical protein FLJ21661	0.61	0.79	1.28
780-781	RAB2L	RAB2, member RAS oncogene family-like	1.05	1.35	1.28
577-579	CD36	CD36	1.26	1.61	1.28
568-570	RYBP	Death effector domain-associated factor=Binds to Caspase 10 DED domain=Homolog of mouse RYBP repressor protein that interacts with Polycomb complex and YY1=YAF2 homolog=DEDAF=YAF2 homolog=MLNewGene3	0.89	1.14	1.28
571-573	ITGAE	CD103 alpha=Integrin alpha-E	1.09	1.38	1.27
		Human SH3 domain-containing protein SH3P18 mRNA, complete cds	1.23	1.56	1.27
755-756	TMEPAI	transmembrane, prostate androgen induced RNA	0.99	1.25	1.26
565-567	NCOA1	SRC-1=steroid receptor coactivator	1.04	1.3	1.25
785	CSNK1E	casein kinase 1, epsilon	0.74	0.92	1.25
768-769	FLJ21940	hypothetical protein FLJ21940	0.91	1.14	1.25
723-724	SAST	syntrophin associated serine/threonine kinase	1.05	1.32	1.25
		ESTs	0.89	1.11	1.25
782-783	GOLGA1	golgi autoantigen, golgin subfamily a, 1	0.76	0.95	1.24
574-576	IL7	IL-7	0.99	1.23	1.24
319	RNAC	RNA cyclase homolog	0.92	1.13	1.24
676-677	KIAA0365	KIAA0365 gene product	0.97	1.2	1.23
679-681	ARHGEF6	KIAA0006	1.04	1.28	1.23
710-711	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	1.11	1.35	1.22
		Unknown	0.9	1.11	1.22
670-671	PON1	paraoxonase 1	0.93	1.14	1.22
		ESTs, Weakly similar to I38588 reverse transcriptase homolog [H.sapiens]	1.11	1.36	1.22
		ESTs	0.72	0.87	1.21
	ATP7A	ATPase, Cu ⁺⁺ transporting, alpha polypeptide (Menkes	0.99	1.2	1.21

		syndrome)			
		Unknown	1.2	1.45	1.21
735-736	CRB1	crumbs (Drosophila) homolog 1	0.88	1.06	1.21
757-758	ZNF211	zinc finger protein 211	0.82	0.99	1.21
		ESTs	0.99	1.16	1.18
685-686	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	0.91	1.07	1.17
687-688	BMP6	bone morphogenetic protein 6	0.95	1.1	1.16
587-588	BAD	BAD=bbc6=proapoptotic Bcl-2 homolog	1.11	0.94	0.85
678	NCSTN	nicastrin	1.13	0.94	0.83
766-767	F23149_1	hypothetical protein F23149_1	1.11	0.91	0.82
701-702	FLJ12442	hypothetical protein FLJ12442	1.04	0.85	0.82
589-591	ZNF173	acid finger protein	1.16	0.95	0.81
741-742	GCAT	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	1.12	0.91	0.81
786-787	AFP	alpha-fetoprotein	1.2	0.96	0.8
		hPAK65=SER/THR-protein kinase PAK-gamma =P21-activated kinase 3	1.05	0.84	0.8
747-748	LOX	lysyl oxidase	0.93	0.75	0.8
662-663	HARS	histidyl-tRNA synthetase	0.73	0.57	0.79
544	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	1.27	1	0.78
697-698	GTPBP1	GP-1=putative G-protein	0.97	0.76	0.78
699-700	GS2NA	nuclear autoantigen	0.96	0.75	0.78
705-706	KIAA0144	KIAA0144 gene product	0.87	0.68	0.78
		Unknown	1.02	0.79	0.78
733-734	PPY2	pancreatic polypeptide 2	1.49	1.16	0.78
653-654	NAGA	N-acetylgalactosaminidase, alpha-	1.06	0.82	0.78
583-584	IL17R	IL-17 receptor	1.05	0.82	0.78
657-658	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na ⁺ /H ⁺ , amiloride sensitive)	0.97	0.75	0.77
691-692	RBBP4	retinoblastoma-binding protein 4	0.87	0.67	0.76
609-611	ILK	ILK=integrin-linked kinase	0.88	0.67	0.76
624-	PTK2B	protein tyrosine kinase PYK2	1.07	0.81	0.76

625					
504-506	AKT1	BPGF-1=bone-derived growth factor=Q6=quiescin=expression is induced by reversible growth arrest, trypsinization and serum starvation and is blocked by SV40 transformation	0.75	0.56	0.75
763-764	DKFZP564C186	DKFZP564C186 protein	0.97	0.73	0.75
554-556	SCYB5	ENA78=chemokine	0.34	0.25	0.75
660-661	MNAT1	menage a trois 1 (CAK assembly factor)	1.24	0.93	0.75
548-550	TCEB2	Elongin B=RNA polymerase II transcription factor SIII p18 subunit	0.98	0.73	0.74
792-793	RBBP2	retinoblastoma-binding protein 2	1.47	1.08	0.74
626-628	MAP2K3	Dual specificity mitogen-activated protein kinase kinase 3	1.06	0.78	0.74
712-713	RALY	RNA-binding protein (autoantigenic)	0.85	0.62	0.74
743-744	P14L	similar to Bos taurus P14 protein	0.87	0.64	0.73
731-732	APMCF1	APMCF1 protein	0.95	0.7	0.73
674-675	GNB2	guanine nucleotide binding protein (G protein), beta polypeptide 2	0.99	0.73	0.73
		Lymphotoxin-Beta receptor precursor=Tumor necrosis factor receptor 2 related protein=Tumor necrosis factor C receptor	1.28	0.93	0.73
		ESTs	1.02	0.73	0.72
666-667	MPI	mannose phosphate isomerase	1.22	0.87	0.71
719-720	PEF	PEF protein with a long N-terminal hydrophobic domain (peflin)	1	0.71	0.71
651-652	FDFT1	farnesyl-diphosphate farnesyltransferase 1	1.09	0.77	0.71
739-740	RAB3A	RAB3A, member RAS oncogene family	0.8	0.57	0.71
		EST	1.49	1.05	0.71
621-623	PPP2R5A	phosphatase 2A B56-alpha (PP2A)	0.89	0.63	0.71
600-602	GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	0.82	0.58	0.7
551-553	NM23H1	nm23-H1=NDP kinase A=Nucleoside diphosphate kinase A	0.71	0.49	0.7
655-656	SECRET	secretagogin	0.84	0.58	0.69

		Unknown	0.8	0.55	0.69
		EST	1.19	0.82	0.69
770-771	FLJ22059	hypothetical protein FLJ22059	0.7	0.49	0.69
659	TUFM	Tu translation elongation factor, mitochondrial	1.16	0.8	0.69
518-520	RUNX1	core binding factor alpha1b subunit=CBF alpha1=PEBP2aA1 transcription factor =AML1 Proto-oncogene=translocated in acute myeloid leukemia	0.69	0.47	0.69
585-586	HGF	Hepatocyte growth factor (hepapoietin A; scatter factor)	0.88	0.6	0.68
		EST, Weakly similar to PRPP_HUMAN SALIVARY PROLINE-RICH PROTEIN II-1 [H.sapiens]	0.98	0.67	0.68
		Unknown	1.02	0.7	0.68
		Human mRNA for unknown product, partial cds	0.57	0.39	0.68
618-620	IL18R1	IL-18 receptor 1=IL-1Rrp	0.88	0.6	0.68
510-512	UBL1	ubiquitin-homology domain protein PIC1	1.49	1.01	0.68
703-704	KIAA0218	KIAA0218 gene product	1.2	0.81	0.68
760-761	MAPRE1	microtubule-associated protein, RP/EB family, member 1	0.6	0.4	0.67
777	SF3B4	splicing factor 3b, subunit 4, 49kD	1.17	0.78	0.67
		Unknown	1.04	0.7	0.67
		ESTs	0.42	0.28	0.66
533	UBE1	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	1.54	1.01	0.66
		Unknown	1.23	0.81	0.66
788-789	COVA1	cytosolic ovarian carcinoma antigen 1	0.57	0.37	0.64
		Unknown	0.82	0.53	0.64
668-669	TAGLN2	transgelin 2	0.7	0.44	0.64
749-750	PISD	phosphatidylserine decarboxylase	0.8	0.5	0.62
775-776	IL1B	interleukin 1, beta	0.3	0.17	0.58
429-430	CALU	calumenin	0.7	0.39	0.56
597-599	PPP1CB	PPP1CB=Protein phosphatase 1, catalytic subunit, beta isoform	0.78	0.44	0.56
751-752		ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens]	0.78	0.43	0.55
745-746	KIAA0008	KIAA0008 gene product	0.49	0.27	0.55
		Unknown	2	1.09	0.54
664-	EIF4A1	eukaryotic translation initiation	0.7	0.37	0.53

665		factor 4A, isoform 1			
559-561	S100A4	S100 calcium binding protein A4=Placental calcium binding protein=Calvasculin=mts1 PROTEIN=CAPL	2.28	1.21	0.53
375	PPIA	peptidylprolyl isomerase A (cyclophilin A)	0.76	0.39	0.52
		EST	2.56	1.26	0.49

Table 10. Markers that can be used to Classify *BRCA1*-like from *BRCA2*-like Tumor Types using Compound Covariate Prediction Analysis.

SEQ ID NO:	Gene	Description	t-value	Average Log ratios in BRCA2 & BRCA2-like sporadics*	Midpoint of average log-ratios in each class	Average log ratios in BRCA1&BRCA1-like sporadic
659	TUFM	Tu translation elongation factor, mitochondrial	-10	-0.09854	-0.016	0.067443
749-750	PISD	phosphatidylserine decarboxylase	8.2305	-0.28567	-0.187	-0.08778
745-746	KIAA0008	KIAA0008 gene product	8.0421	-0.56864	-0.431	-0.29414
703-704	KIAA0218	KIAA0218 gene product	7.9288	-0.08197	-0.005	0.071882
751-752	EST	ESTs, Weakly similar to A Chain A, Cyclophilin A [H.sapiens]	7.6225	-0.34775	-0.225	-0.10292
621-623	PPP2R5A	phosphatase 2A B56-alpha (PP2A)	-7.469	-0.20343	-0.121	-0.03763
733-734	PPY2	pancreatic polypeptide 2	7.3866	0.06558	0.113	0.160168
649	EST	Unknown	-7.384	-0.27327	-0.183	-0.09313
641	EST	EST, Weakly similar to PRPP_HUMAN SALIVARY PROLINE-RICH PROTEIN II-1 [H.sapiens]	7.3561	-0.17457	-0.095	-0.01592
375	PPIA	peptidylprolyl isomerase A (cyclophilin A)	6.9946	-0.38934	-0.258	-0.12668
770-771	FLJ22059	hypothetical protein FLJ22059	6.9726	-0.31605	-0.228	-0.14026
739	RAB3A	RAB3A, member RAS oncogene family	6.9458	-0.23582	-0.167	-0.098
655-656	SECRET	secretagogin	6.9307	-0.23657	-0.147	-0.0575
629-631	TNFR2RP	Lymphotoxin-Beta receptor precursor=Tumor necrosis factor receptor 2 related protein=Tumor necrosis factor C receptor	6.9268	-0.02733	0.038	0.103462
551-553	NM23H1	nm23-H1=NDP kinase A=Nucleoside diphosphate kinase A	6.8307	-0.32239	-0.242	-0.16241
557-558	PAK2	hPAK65=SER/THR-protein kinase PAK-gamma =P21-activated kinase 3	6.7214	-0.1152	-0.05	0.01536
806	APRT	adenine phosphoribosyltransferase	6.6725	0.044932	0.085	0.125156
807-808	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	-6.648	-0.21681	-0.144	-0.0716
544	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	6.6083	0.003461	0.047	0.089905

719-720	PEF	PEF protein with a long N-terminal hydrophobic domain (peflin)	6.6034	-0.16368	-0.088	-0.01144
747-748	LOX	lysyl oxidase	6.4441	-0.12784	-0.077	-0.02641
775-776	IL1B	interleukin 1, beta	6.4272	-0.75203	-0.637	-0.52288
809-810	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	-6.425	-0.10347	-0.048	0.007748
653-654	NAGA	N-acetylgalactosaminidase, alpha-	-6.42	-0.09205	-0.034	0.024896
760-761	MAPRE1	microtubule-associated protein, RP/EB family, member 1	-6.39	-0.39254	-0.296	-0.19928
811-812	ARD1	N-acetyltransferase, homolog of <i>S. cerevisiae</i> ARD1	6.3833	-0.1707	-0.11	-0.04915
813-814	CDC6	CDC6 (cell division cycle 6, <i>S. cerevisiae</i>) homolog	-6.371	-0.25964	-0.201	-0.14327
643	EST	EST	6.3541	0.133858	0.253	0.371068
583-584	IL17R	IL-17 receptor	6.3499	-0.08991	-0.035	0.019532
803	WNT5B	wingless-type MMTV integration site family, member 5B	6.3391	-0.06803	-0.017	0.035029
651-652	FDFT1	farnesyl-diphosphate farnesyltransferase 1	6.3387	-0.1152	-0.038	0.039414
664-665	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	6.2705	-0.39362	-0.263	-0.13253
650	EST	Unknown	6.2573	-0.08355	-0.002	0.079181
657-658	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na ⁺ /H ⁺ , amiloride sensitive)	6.2571	-0.13608	-0.077	-0.01682
731-732	APMCF1	APMCF1 protein	6.2387	-0.15677	-0.083	-0.00922
503	ZNF220	zinc finger protein 220	6.2316	-0.13549	-0.072	-0.00922
815-816	PTPRCAP	LPAP=lymphoid-restricted phosphoprotein=CD45 phosphatase binding protein and putative substrate	-6.229	-0.10182	-0.059	-0.01592
817	POLD3	polymerase (DNA directed), delta 3	-6.223	-0.29843	-0.221	-0.14327
788-789	COVA1	cytosolic ovarian carcinoma antigen 1	6.1802	-0.42946	-0.321	-0.21325
701-702	FLJ12442	hypothetical protein FLJ12442	6.1607	-0.07676	-0.027	0.023252
818	EST	Unknown	6.1033	-0.12494	-0.057	0.011993
721-722	EST	Human mRNA for unknown product, partial cds	6.1032	-0.40671	-0.328	-0.24949
662-	HARS	histidyl-tRNA synthetase	-	-0.24642	-0.186	-0.12552

663			6.0889			
819	FLJ20746	putative cyclin G1 interacting protein	-			
			6.0827	-0.04144	0.017	0.074451
820-821	PLK	pLK=homologue of Drosophila polo serine/threonine kinase	-			
			6.0725	-0.32422	-0.253	-0.18177
784	TNRC12	trinucleotide repeat containing 12	6.0744	0.110253	0.062	0.01368
723-724	SAST	syntrophin associated serine/threonine kinase	6.0991	0.107549	0.065	0.022016
634-635	EST	ESTs	6.1178	0.048053	-0.002	-0.05306
695-696	SMG1	PI-3-kinase-related kinase SMG-1	6.1219	0.146438	0.087	0.028571
534-535	LOC51760	B/K protein	6.1306	0.09691	0.048	-0.00174
574-576	IL7	IL-7	6.1558	0.088845	0.043	-0.00305
670-671	PON1	paraoxonase 1	6.3314	0.058046	0.014	-0.03105
592-593	ZFP161	ZF5=POZ domain zinc finger protein	6.3356	0.196176	0.101	0.006466
632-633	EST	ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	6.3426	0.028978	-0.029	-0.08725
765		ESTs	6.4363	0.026533	-0.03	-0.08619
822	CCR6	CCR6=STRL22=chemokine receptor for MIP-3 alpha/LARC/Exodus on activated B cells	6.4897	0.116276	0.069	0.022016
679-681	ARHGEF6	KIAA0006	6.5098	0.105169	0.065	0.024075
759	LOC51605	CGI-09 protein	6.662	0.0086	-0.042	-0.09205
762	FLJ10701	hypothetical protein FLJ10701	6.925	0.135133	0.075	0.0141
636	EST	Unknown	7.3197	0.050766	0.005	-0.04144
647	EST	EST	7.5484	0.045714	-0.012	-0.07007
725-726	EST	Unknown	8.058	0.068557	-0.006	-0.07988

Table 11. Results of Compound Covariate Predictor Analysis.

Expld	Pre-specified class label	Correctly classified
B2-1 vs OSE B2-1 vs OSE 21083	1	YES
B2-10 vs OSE B2-10 vs OSE 21085	1	YES
B2-16 vs OSE B2-16 vs OSE 21180	1	YES
B2-2 vs OSE B2-2 vs OSE 21090	1	YES
B2-20 vs OSE B2-20 vs OSE	1	YES

21181		
B2-21 vs OSE B2-21 vs OSE 21182	1	YES
B2-22 vs OSE B2-22 vs OSE 21183	1	YES
B2-23 vs OSE B2-23 vs OSE 21091	1	YES
B2-24 vs OSE B2-24 vs OSE 21092	1	NO
B2-25 vs OSE B2-25 vs OSE 22038	1	YES
B2-3 vs OSE B2-3 vs OSE 21093	1	YES
B2-4 vs OSE B2-4 vs OSE 21094	1	YES
B2-5 vs OSE B2-5 vs OSE 21095	1	NO
B2-7 vs OSE B2-7 vs OSE 21096	1	YES
B2-8 vs OSE B2-8 vs OSE 21097	1	YES
B2-9 vs OSE B2-9 vs OSE 21098	1	YES
C100 vs OSE C100 vs OSE 21167	1	YES
C102 vs OSE C102 vs OSE 21168	1	YES
C103 vs OSE C103 vs OSE 21169	1	YES
C105 vs OSE C105 vs OSE 21178	1	YES
C107 vs OSE C107 vs OSE 21099	1	YES
C110 vs OSE C110 vs OSE 21101	1	YES
C111 vs OSE C111 vs OSE 21102	1	NO
C117 vs OSE C117 vs OSE 21105	1	YES
C118 vs OSE C118 vs OSE 21106	1	YES
C123 vs OSE C123 vs OSE 21107	1	YES
C46 vs OSE C46 vs OSE 19741	1	NO
C77 vs OSE C77 vs OSE 21108	1	YES
C84 vs OSE C84 vs OSE 21368	1	YES
C85 vs OSE C85 vs OSE 21179	1	YES
C99 vs OSE C99 vs OSE 21370	1	YES
B36 vs OSE B36 vs OSE 19680	2	YES
B39 vs OSE B39 vs OSE 19682	2	YES
B40 vs OSE B40 vs OSE 19683	2	YES
B41 vs OSE B41 vs OSE 19684	2	YES
B52-2 vs OSE B52-2 vs OSE 19771	2	NO
B54 vs OSE B54 vs OSE 19687	2	YES
B55 vs OSE B55 vs OSE 19688	2	YES
B60 vs OSE B60 vs OSE 19690	2	YES
B61 vs OSE B61 vs OSE 19695	2	YES
B62 vs OSE B62 vs OSE 19701	2	YES

B63 vs OSE B63 vs OSE 19706	2	YES
B64 vs OSE B64 vs OSE 19713	2	YES
B70 vs OSE B70 vs OSE 19722	2	YES
B74 vs OSE B74 vs OSE 19727	2	YES
B77 vs OSE B77 vs OSE 19731	2	YES
B78 vs OSE B78 vs OSE 21103	2	YES
B79 vs OSE B79 vs OSE 19743	2	YES
B80 vs OSE B80 vs OSE 21088	2	YES
C114 vs OSE C114 vs OSE 21104	2	YES
C15 vs OSE C15 vs OSE 19734	2	YES
C16 vs OSE C16 vs OSE 19735	2	YES
C17 vs OSE C17 vs OSE 19736	2	YES
C1 vs OSE C1 vs OSE 19732	2	YES
C20 vs OSE C20 vs OSE 19737	2	YES
C41 vs OSE C41 vs OSE 19739	2	YES
C42 vs OSE C42 vs OSE 19740	2	YES
C49 vs OSE C49 vs OSE 19742	2	YES
C79 vs OSE C79 vs OSE 21367	2	YES
C87 vs OSE C87 vs OSE 19744	2	YES
C95 vs OSE C95 vs OSE 21369	2	YES
Overall Success		91.80%